

Gln Met Ile Ser Gln Gly Ala Ser Lys Val Asn Met Ser Leu Ile Val
 50 55 60

His Asp Ser Asp Ala Lys Ala Leu Val Glu Ala Leu His Gln Ala Phe
 65 70 75 80

Phe Glu Asp Asp Val Leu Ser Gln Val Glu Ala Glu Asn Leu Leu Val
 85 90 95

Gly

<210> 3
 <211> 513
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (474)

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 acccgaaccg ggcctcgccgg tgcaagaggg ttgtcaatgg tggtcgccga ctccaccagc 180
 cgtcggggcca agcaagcggc cggcggggac ggcgtccctt gggccctgt tctcggaggg 240
 ctcggatgg agggattggg gatcagctc agcgtggta tgaagttcgg ggggtcctcg 300
 gtgtcgatgg cccgcaggat ggctgaggtg gccggccctca tcctgacgtt ccccgaggag 360
 cgcccccgtcg tcgttctctc tgccatgggg aaaaccacca acaaccttct ccttgctggg 420
 agaaaaggca ataaggtgtg gagttatcat gtttctgaa atccgaagaa tggnatatgg 480
 tcaaaaagcc taaaatatca aagtatccca act 513

<210> 4
 <211> 152
 <212> PRT
 <213> Zea mays

<400> 4
 Thr Glu Gln Glu Asp Ser Glu Met Ala Ile Pro Val Arg Ser Ala Ala
 1 5 10 15

Ala Pro Arg Arg Leu Val Pro Ser Ile Pro Pro Ala Ser Ser Gly His
 20 25 30

Val Arg Gly Leu Ala Cys Phe Gly Thr Arg Thr Gly Pro Arg Gly Ala
 35 40 45

Arg Gly Leu Ser Met Val Val Ala Asp Ser Thr Ser Arg Arg Ala Lys
 50 55 60

Gln Ala Asp Gly Gly Asp Gly Val Leu Gly Ala Pro Val Leu Gly Gly
 65 70 75 80

Leu Gly Met Glu Gly Leu Gly Asp Gln Leu Ser Val Val Met Lys Phe
 85 90 95

Gly Gly Ser Ser Val Ser Ser Ala Ala Arg Met Ala Glu Val Ala Gly
 100 105 110

Leu Ile Leu Thr Phe Pro Glu Glu Arg Pro Val Val Val Leu Ser Ala
 115 120 125

Met Gly Lys Thr Thr Asn Asn Leu Leu Leu Ala Gly Arg Lys Gly Asn
 130 135 140

Lys Val Trp Ser Tyr His Val Phe
 145 150

<210> 5
 <211> 1985
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (532)

<220>
 <221> unsure
 <222> (1180)

<400> 5
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 cttcggtacc cgaaccgggc ctcgcgggtgc aagagggttgc tcaatgggtgg tcgcccactc 180
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 gcctaggacc agtgactacc ttgtttcatt tggagaatgc atgtccacca ggatttttc 660
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 gaagagactt catggggact ggatacagga tccagcgata cctgttggta ctgggttcct 840
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 tgctacaacc atttgtttaag ctttgggact gagagaaaattt caggtatggaa aagatgttga 960
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 atttgaagag gcccacagaac ttgttttattt tgggtgttac gttttgcatac cacaatcgat 1080
 gagacactgtc agagaagggtt atattccatgt tagggtaaattt aattcataca accctaaac 1140
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 aatagcaattt gttcgatctac ttccgtcaggag ggcgataattt tcactatcg gaaatgttga 1500
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<210> 6
 <211> 560
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (168)

<220>
 <221> UNSURE
 <222> (384)

<400> 6
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 Ser Ile Pro Pro Ala Ser Ser Gly His Val Arg Gly Leu Ala Cys Phe
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 35 40 45
 Ala Asp Ser Thr Ser Arg Arg Ala Lys Gln Ala Asp Gly Gly Asp Gly
 50 55 60
 Val Leu Gly Ala Pro Val Leu Gly Gly Leu Gly Met Glu Gly Leu Gly
 65 70 75 80
 Asp Gln Leu Ser Val Val Met Lys Phe Gly Gly Ser Ser Val Ser Ser
 85 90 95
 Ala Ala Arg Met Ala Glu Val Ala Gly Leu Ile Leu Thr Phe Pro Glu
 100 105 110
 Glu Arg Pro Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn Asn
 115 120 125
 Leu Leu Leu Ala Gly Glu Lys Ala Val Gly Cys Gly Val Ile His Val
 130 135 140
 Ser Glu Ile Glu Glu Trp Asn Met Val Lys Ser Leu His Ile Lys Thr
 145 150 155 160
 Val Asp Glu Leu Gly Leu Pro Xaa Ile Cys Asn Thr Ser Leu Tyr Glu
 165 170 175
 Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu Thr Pro
 180 185 190
 Arg Thr Ser Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg
 195 200 205
 Ile Phe Ser Ala Tyr Leu Asn Lys Ile Arg Val Lys Ala Arg Gln Tyr
 210 215 220
 Asp Ala Phe Asp Ile Gly Phe Ile Thr Thr Asp Glu Phe Gly Asn Ala
 225 230 235 240

Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His Gly
 245 250 255

Asp Trp Ile Gln Asp Pro Ala Ile Pro Val Val Thr Gly Phe Leu Gly
 260 265 270

Lys Gly Trp Lys Ser Gly Ala Val Thr Thr Leu Gly Arg Gly Ser
 275 280 285

Asp Leu Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu Ile
 290 295 300

Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn Ile
 305 310 315 320

Tyr Pro His Ala Lys Thr Val Pro Tyr Leu Thr Phe Glu Glu Ala Thr
 325 330 335

Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met Arg
 340 345 350

Pro Ala Arg Glu Gly Asp Ile Pro Val Arg Val Lys Asn Ser Tyr Asn
 355 360 365

Pro Lys Ala Pro Gly Thr Leu Ile Thr Arg Gln Arg Asp Met Asp Xaa
 370 375 380

Gly Leu Val Val Leu Thr Ser Ile Val Leu Lys Ser Asn Val Thr Met
 385 390 395 400

Leu Asp Ile Val Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala
 405 410 415

Arg Val Ser Gly Ile Cys Tyr Ile Glu Asp Leu Cys Ile Ser Val Asp
 420 425 430

Cys Val Ala Thr Ser Glu Val Ser Val Ser Val Ser Leu Asp Pro Ser
 435 440 445

Lys Ile Trp Ser Arg Glu Leu Ile Gln Gln Ala Ser Glu Leu Asp His
 450 455 460

Val Val Glu Glu Leu Glu Lys Ile Ala Ile Val Arg Leu Leu Gln Gln
 465 470 475 480

Arg Ala Ile Ile Ser Leu Ile Gly Asn Val Glu Gln Ser Ser Leu Ile
 485 490 495

Leu Glu Lys Thr Gly Arg Val Leu Arg Lys Ser Gly Val Asn Val Gln
 500 505 510

Met Ile Ser Gln Gly Ala Ser Lys Val Asn Met Ser Leu Ile Val His
 515 520 525

Asp Ser Asp Ala Lys Ala Leu Val Glu Ala Leu His Gln Ala Phe Phe
 530 535 540

Glu Asp Asp Val Leu Ser Gln Val Glu Ala Glu Asn Leu Leu Val Gly
 545 550 555 560

<210> 7
<211> 1953
<212> DNA
<213> Zea mays

<400> 7

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cgaaccgggc	ctcgcggtgc	aagagggttg	tcaatggtg	tcggcgactc	caccagccgt	180
cggggcaagc	aagcggacgg	cggggacggc	gtccttgggg	cgcctgttct	cggagggctc	240
gggatggagg	gattggggga	tcagctcage	gtgggtgatga	agttcggggg	gtcctcggtg	300
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cccgctgtcg	ttctctctgc	catggggaaa	accaccaaca	accttctct	tgctggagag	420
aaggcagttag	ggtgtggagt	tatccatgtt	tctgaatcg	aagagtggaa	tatgtcaaa	480
agcctacata	tcaagacggg	ggatgaactt	ggacttccaa	gatctgtat	acaagacatg	540
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accagtgact	accttggttc	atttggagaa	tgcatgtcca	ccaggatttt	ttctgcttat	660
ttgaacaaaa	ttcgtgtcaa	ggcacggcag	tatgacgcat	ttgatattgg	tttcattaca	720
actgatgaat	ttggtaatgc	ggatatactt	gaagcaacct	atccctgtgt	tgcgaagaga	780
cttcatgggg	actggataca	ggatccagcg	ataccctgtt	ttactgggtt	ccttgggaag	840
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accattggta	aaggcttggg	actgagagaa	attcaggtat	ggaaagatgt	tgtatggtga	960
cttacttgtg	atccaaatat	ctaccacat	gcaaaagactg	ttccatactt	aacatttga	1020
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gctagagaag	gtgatattcc	agttagggtt	aagaattcat	acaaccctaa	agctccaggc	1140
acccttatta	ccagacaaaag	agacatggat	agggtgtac	taactagcat	agtgtcaag	1200
tcaaatgtca	ctatgttgg	catttgagc	actcggatgc	ttggtcagta	tggtttctg	1260
gcaagggtat	ttgctatatt	tgaagatcta	tgtatatctg	tggattgtgt	tgctaccagt	1320
gaagtttagt	tttctgtgtc	acttgatcca	tcaaagatct	ggagtaggg	actgatacag	1380
caggaacttg	accatgttagt	tgaagagctt	gagaaaataag	caattgttcg	tctacttcag	1440
cagagggcga	taatttcact	tatcgaaat	gtggagcaat	cgtctctcat	actagaaaag	1500
acgggacgtg	tgctgaggaa	aagtggggtt	aatgttcaga	tgatctcgca	aggagcgtca	1560
aaggtaaca	tgtcgctgtat	agtccatgtat	agcgatgcaa	aggcactcgt	agaagccctt	1620
catcaggcgt	tcttgaaga	cgatgtccta	tcacaagtcg	aagcggagaa	cctactcg	1680
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ttccaggtt	tcaagccatg	actgcggaaac	tgtgtttctg	ttttagaact	gttgcagac	1860
accagtgagc	tgcgagcacc	gattgtcaac	aagatggcaa	gcctgtgata	taattccaa	1920
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<210> 8
<211> 555
<212> PRT
<213> Zea mays

<400>

Met Ala Ile Pro Val Arg Ser Ala Ala Ala Pro Arg Arg Leu Val Pro
1 5 10 15

Ser Ile Pro Pro Ala Ser Ser Gly His Val Arg Gly Leu Ala Cys Phe
20 25 30

Gly Thr Arg Thr Gly Pro Arg Gly Ala Arg Gly Leu Ser Met Val Val
35 40 45

Ala Asp Ser Thr Ser Arg Arg Ala Lys Gln Ala Asp Gly Gly Asp Gly
50 55 60

Val Leu Gly Ala Pro Val Leu Gly Gly Leu Gly Met Glu Gly Leu Gly
 65 70 75 80

Asp Gln Leu Ser Val Val Met Lys Phe Gly Gly Ser Ser Val Ser Ser
 85 90 95

Ala Ala Arg Met Ala Glu Val Ala Gly Leu Ile Leu Thr Phe Pro Glu
 100 105 110

Glu Arg Pro Val Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn Asn
 115 120 125

Leu Leu Leu Ala Gly Glu Lys Ala Val Gly Cys Gly Val Ile His Val
 130 135 140

Ser Glu Ile Glu Glu Trp Asn Met Val Lys Ser Leu His Ile Lys Thr
 145 150 155 160

Val Asp Glu Leu Gly Leu Pro Arg Ser Val Ile Gln Asp Met Leu Asp
 165 170 175

Glu Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu Thr
 180 185 190

Pro Arg Thr Ser Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr
 195 200 205

Arg Ile Phe Ser Ala Tyr Leu Asn Lys Ile Arg Val Lys Ala Arg Gln
 210 215 220

Tyr Asp Ala Phe Asp Ile Gly Phe Ile Thr Thr Asp Glu Phe Gly Asn
 225 230 235 240

Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His
 245 250 255

Gly Asp Trp Ile Gln Asp Pro Ala Ile Pro Val Val Thr Gly Phe Leu
 260 265 270

Gly Lys Gly Trp Lys Ser Gly Ala Val Thr Thr Leu Gly Arg Gly Gly
 275 280 285

Ser Asp Leu Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu
 290 295 300

Ile Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn
 305 310 315 320

Ile Tyr Pro His Ala Lys Thr Val Pro Tyr Leu Thr Phe Glu Glu Ala
 325 330 335

Thr Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met
 340 345 350

Arg Pro Ala Arg Glu Gly Asp Ile Pro Val Arg Val Lys Asn Ser Tyr
 355 360 365

Asn Pro Lys Ala Pro Gly Thr Leu Ile Thr Arg Gln Arg Asp Met Asp
 370 375 380

Lys Val Val Leu Thr Ser Ile Val Leu Lys Ser Asn Val Thr Met Leu
385 390 395 400

Asp Ile Val Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala Arg
405 410 415

Val Phe Ala Ile Phe Glu Asp Leu Cys Ile Ser Val Asp Cys Val Ala
420 425 430

Thr Ser Glu Val Ser Val Ser Leu Asp Pro Ser Lys Ile Trp
435 440 445

Ser Arg Glu Leu Ile Gln Gln Glu Leu Asp His Val Val Glu Glu Leu
450 455 460

Glu Lys Ile Ala Ile Val Arg Leu Leu Gln Gln Arg Ala Ile Ile Ser
465 470 475 480

Leu Ile Gly Asn Val Glu Gln Ser Ser Leu Ile Leu Glu Lys Thr Gly
485 490 495

Arg Val Leu Arg Lys Ser Gly Val Asn Val Gln Met Ile Ser Gln Gly
500 505 510

Ala Ser Lys Val Asn Met Ser Leu Ile Val His Asp Ser Asp Ala Lys
515 520 525

Ala Leu Val Glu Ala Leu His Gln Ala Phe Phe Glu Asp Asp Val Leu
530 535 540

Ser Gln Val Glu Ala Glu Asn Leu Leu Val Gly
545 550 555

<210> 9

<211> 455

<212> DNA

<213> Oryza sativa

<220>

<221> unsure

<222> (366)

<220>

<221> unsure

<222> (394)

<220>

<221> unsure

<222> (406)

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<221> unsure

<222> (414)

<220>

<221> unsure

<222> (425)

<220>
<221> unsure
<222> (431)

<220>
<221> unsure
<222> (455)

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aatccaatca ccctgttaacc tctttgcaac agcaggatat gtcgcttcaa gaatgtccgc 180
atttgtgaaa tcatcagtag ttataaagcc aatatcaa at gcatcatact gccgagcctt 240
tttcccaagt ttattcaa atgcaagcaa atattctgt agacatgcat tcaccgaagg 300
aaacaaggtt atccccgtgtc ctaaggagtt aagttcttc aatcaatagc aacaccctta 360
aagaangttt gttccaaattc cttccaaata aaanccttga aacaantccg gatnctaatac 420
ccaantccca nacgcctcata aaatttagtcc ctaan 455

<210> 10
<211> 114
<212> PRT
<213> Oryza sativa

<400> 10
Leu Lys Glu Leu Asn Ser Leu Gly His Gly Ile Thr Leu Phe Pro Ser
1 5 10 15

Val Asn Ala Cys Leu Gln Glu Tyr Leu Leu Ala Tyr Leu Asn Lys Leu
20 25 30

Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Ile Gly Phe Ile Thr
35 40 45

Thr Asp Asp Phe Thr Asn Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala
50 55 60

Val Ala Lys Arg Leu Gln Gly Asp Trp Ile Asp Asp Pro Ala Ile Pro
65 70 75 80

Ile Val Thr Gly Phe Leu Gly Lys Gly Trp Lys Ser Cys Ala Val Thr
85 90 95

Thr Leu Gly Arg Gly Gly Ser Asp Leu Thr Ala Thr Thr Ile Gly Lys
100 105 110

Ala Leu

<210> 11
<211> 847
<212> DNA
<213> Oryza sativa

<400> 11
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gaggggatgtg ttccgaggagg aggggatgg tggtgccgtg ccagagcggg gcggcggcgg 120
ttgtcctcaa caaggacgac gccgcgtcg tggccgcccgc cgccgcctcc tccgcgacgg 180
ggttcaccgt cgccatgaag ttccggcggt cgtcggtggc gtcggcggag cggatgcggg 240

aggtgtggccga tctcatactc agcttccccg aggagactcc cgttgttgtt ctctccgcca 300
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 cgaaggcgtc taaaaattccc gagctcgag ttatcaagga gctccatgtt aggactattg 420
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 ttaagggtgt tgctatgtg aaagaactaa ctcctaggac acgggattac cttgtttcct 540
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 cgcgtgg 847

<210> 12
 <211> 281
 <212> PRT
 <213> Oryza sativa

<400> 12

Pro Pro Arg Val Gly Arg Glu Gln Gln Tyr Leu Ala Cys Ala Ala Ala
 1 5 10 15

Ala Arg Pro Gly Gly Arg Cys Ser Arg Arg Arg Gly Leu Val Val Arg
 20 25 30

Cys Gln Ser Gly Ala Ala Ala Val Val Leu Asn Lys Asp Asp Ala Ala
 35 40 45

Ser Val Ala Ala Ala Ala Ser Ser Ala Thr Gly Phe Thr Val Ala
 50 55 60

Met Lys Phe Gly Gly Ser Ser Val Ala Ser Ala Glu Arg Met Arg Glu
 65 70 75 80

Val Ala Asp Leu Ile Leu Ser Phe Pro Glu Glu Thr Pro Val Val Val
 85 90 95

Leu Ser Ala Met Gly Lys Thr Thr Asn Asn Leu Leu Leu Ala Gly Glu
 100 105 110

Lys Ala Val Ser Cys Gly Ala Pro Lys Ala Ser Glu Ile Pro Glu Leu
 115 120 125

Ala Val Ile Lys Glu Leu His Val Arg Thr Ile Asp Glu Leu Gly Leu
 130 135 140

Asp Arg Ser Ile Val Ser Gly Leu Leu Glu Leu Glu Gln Leu Leu
 145 150 155 160

Lys Gly Val Ala Met Met Lys Glu Leu Thr Pro Arg Thr Arg Asp Tyr
 165 170 175

Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe Ala Ala Tyr
 180 185 190

Leu Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Ile
 195 200 205

Gly Phe Ile Thr Thr Asp Asp Phe Thr Asn Ala Asp Ile Leu Glu Ala
 210 215 220

Thr Tyr Pro Ala Val Ala Lys Arg Leu Gln Gly Asp Trp Ile Asp Asp
225 230 235 240
Pro Ala Ile Pro Ile Val Thr Gly Phe Leu Gly Lys Gly Trp Lys Ser
245 250 255
Cys Ala Val Thr Thr Leu Gly Arg Gly Ser Asp Leu Thr Ala Thr
260 265 270
Thr Ile Gly Lys Ala Leu Arg Thr Arg
275 280

<210> 13
<211> 646
<212> DNA
<213> *Triticum aestivum*

<220>
<221> unsure
<222> (289)

<220>
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<220>
<221> unsure
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<220>
<221> unsure
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<220>
<221> unsure
<222> (582)...(583)

<220>
<221> unsure
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<220>
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<220>
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<220>
<221> unsure
<222> (637)

PCT/US00/34396

<220>
 <221> unsure
 <222> (640)

<400> 13
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 acgagattac ctgtttccct ttggtaatg catgtctaca agaatatttt ctgcataattt 240
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 tggacgattt ccacaaatgc cgatatccnc gaacaactta tcctgctgtt gcaaagagct 360
 acatggaaat tgggtatgat ccctgctatc ccnatatgac gttcccttg ggaaggatg 420
 gaacttgtgc ggcanaactt aggaaggggc ggaatgactt gacggcacaa ccatgggaaa 480
 cctgggtta agaaaatca gttggaaat gtaacggtt tgactgtat caatattatc 540
 aaaccggaca ntaccactta cttttaggg accgaacttc tnnttgaa agtttgcacca 600
 tcatacacacc aggagngacc cattcntaaa cnnaacntcn cccgga 646

<210> 14
 <211> 146
 <212> PRT
 <213> *Triticum aestivum*

<220>
 <221> UNSURE
 <222> (110)

<220>
 <221> UNSURE
 <222> (131)

<220>
 <221> UNSURE
 <222> (145)

<400> 14
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 Val Ile Lys Glu Leu His Leu Arg Thr Ile Asp Glu Leu Gly Leu Asp
 20 25 30
 Ser Ser Ile Val Ser Gly Phe Leu Asp Glu Leu Glu Gln Leu Leu Lys
 35 40 45
 Gly Val Ala Met Met Lys Glu Leu Thr Leu Arg Thr Arg Asp Tyr Leu
 50 55 60
 Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe Ser Ala Tyr Leu
 65 70 75 80
 Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala Phe Asp Leu Gly
 85 90 95
 Phe Ile Thr Thr Gly Arg Phe Pro Gln Met Pro Ile Ser Xaa Asn Asn
 100 105 110
 Leu Ser Cys Cys Cys Lys Glu Leu His Gly Asn Trp Leu Met Thr Leu
 115 120 125

Leu Ser Xaa Tyr Asp Gly Ser Leu Gly Lys Gly Trp Asn Leu Cys Gly
130 135 140

Xaa Thr
145

<210> 15
<211> 1658
<212> DNA
<213> *Triticum aestivum*

<400> 15

<210> 16
<211> 439
<212> PRT
<213> *Triticum aestivum*

<400> 16
Phe Gly Thr Arg Ala Val Ser Cys Gly Ala Pro Lys Ala Ser Glu Ile
1 5 10 15

Tyr Glu Leu Ala Val Ile Lys Glu Leu His Leu Arg Thr Ile Asp Glu
20 25 30

Leu Gly Leu Asp Ser Ser Ile Val Ser Gly Phe Leu Asp Glu Leu Glu
35 40 45

Gln Leu Leu Lys Gly Val Ala Met Met Lys Glu Leu Thr Leu Arg Thr
50 55 60

Arg Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser Thr Arg Ile Phe
 65 70 75 80
 Ser Ala Tyr Leu Asn Lys Leu Gly Lys Lys Ala Arg Gln Tyr Asp Ala
 85 90 95
 Phe Asp Leu Gly Phe Ile Thr Thr Asp Asp Phe Thr Asn Ala Asp Ile
 100 105 110
 Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu His Gly Asp Trp
 115 120 125
 Ile Asp Asp Pro Ala Ile Pro Ile Val Thr Gly Phe Leu Gly Lys Gly
 130 135 140
 Trp Lys Ser Cys Ala Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Leu
 145 150 155 160
 Thr Ala Thr Thr Ile Gly Lys Ala Leu Gly Leu Arg Glu Ile Gln Val
 165 170 175
 Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro Asn Ile Tyr Ala
 180 185 190
 Asn Ala Val Pro Val Pro Tyr Leu Thr Phe Asp Glu Ala Ala Glu Leu
 195 200 205
 Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser Met Arg Pro Ala
 210 215 220
 Arg Glu Gly Gly Ile Pro Val Arg Val Lys Asn Ser Tyr Asn Arg His
 225 230 235 240
 Ala Pro Gly Thr Val Ile Thr Lys Thr Arg Asp Met Arg Lys Ser Ile
 245 250 255
 Leu Thr Ser Ile Val Leu Lys Ser Asn Ile Thr Met Leu Asp Ile Val
 260 265 270
 Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala Lys Val Phe Ser
 275 280 285
 Ile Phe Glu Asp Leu Gly Ile Ser Val Asp Ser Val Ala Thr Ser Glu
 290 295 300
 Val Ser Ile Ser Leu Thr Leu Asp Pro Ser Lys Leu Trp Ser Arg Glu
 305 310 315 320
 Leu Ile Gln Gln Glu Leu Asp His Val Val Glu Glu Leu Glu Lys Ile
 325 330 335
 Ala Val Val His Leu Leu Gln His Arg Ser Ile Ile Ser Leu Ile Gly
 340 345 350
 Asn Val Gln Arg Ser Ser Leu Ile Leu Glu Lys Ala Phe Asn Val Leu
 355 360 365
 Arg Arg Asn Gly Val Asn Val Gln Met Ile Ser Gln Gly Ala Ser Lys
 370 375 380

Val Asn Ile Ser Leu Val Val Asn Asp Ser Glu Ala Lys Gln Cys Val
 385 390 395 400
 Gln Ala Leu His Ser Ala Phe Phe Glu Asn Gly Phe Leu Ser Glu Val
 405 410 415
 Glu Glu Ala Asp Leu Ala Gln Lys Arg Ala Pro Val Leu Val Ser Ser
 420 425 430
 Asn Gly Ala Ile Asn Gly Asn
 435

<210> 17
 <211> 564
 <212> PRT
 <213> Glycine max

<400> 17
 Met Ala Ser Ala Leu Gln Gln Leu Gln Gly Val Gln Gly Lys Leu Ala
 1 5 10 15
 Val Ser Met Ser Val Arg Arg Ser Leu His His Cys Lys Ser Gln Ile
 20 25 30
 Gly Phe Ala Ala Leu Gly Ala Pro Val Cys Ala Arg Arg Val Trp Gly
 35 40 45
 Asn Arg Val Ala Phe Ser Val Thr Thr Cys Lys Ala Ser Thr Ser Asp
 50 55 60
 Val Ile Glu Lys Asn Ala Thr Glu Asn Gly Met Val Ser Ser Glu Gly
 65 70 75 80
 Glu Thr Ser Phe Thr Cys Val Met Lys Phe Gly Gly Ser Ser Val Ala
 85 90 95
 Ser Ala Asp Arg Met Lys Glu Val Ala Thr Leu Ile Leu Ser Phe Pro
 100 105 110
 Glu Glu Arg Pro Ile Val Val Leu Ser Ala Met Gly Lys Thr Thr Asn
 115 120 125
 Lys Leu Leu Ala Gly Glu Lys Ala Val Ser Cys Gly Val Ile Asn
 130 135 140
 Val Ser Ser Ile Glu Glu Leu Cys Phe Ile Lys Asp Leu His Leu Arg
 145 150 155 160
 Thr Val Asp Gln Leu Gly Val Asp Gly Ser Val Ile Ser Lys His Leu
 165 170 175
 Glu Glu Leu Glu Gln Leu Leu Lys Gly Ile Ala Met Met Lys Glu Leu
 180 185 190
 Thr Lys Arg Thr Gln Asp Tyr Leu Val Ser Phe Gly Glu Cys Met Ser
 195 200 205

Thr Arg Ile Phe Ala Ala Tyr Leu Asn Lys Ile Gly Val Lys Ala Arg
 210 215 220
 Gln Tyr Asp Ala Phe Glu Ile Gly Phe Ile Thr Thr Asp Asp Phe Thr
 225 230 235 240
 Asn Ala Asp Ile Leu Glu Ala Thr Tyr Pro Ala Val Ala Lys Arg Leu
 245 250 255
 His Gly Asp Trp Leu Ser Asp Pro Ala Ile Ala Ile Val Thr Gly Phe
 260 265 270
 Leu Gly Lys Ala Arg Lys Ser Cys Ala Val Thr Thr Leu Gly Arg Gly
 275 280 285
 Gly Ser Asp Leu Thr Ala Thr Ile Gly Lys Ala Leu Gly Leu Pro
 290 295 300
 Glu Ile Gln Val Trp Lys Asp Val Asp Gly Val Leu Thr Cys Asp Pro
 305 310 315 320
 Asn Ile Tyr Pro Lys Ala Glu Pro Val Pro Tyr Leu Thr Phe Asp Glu
 325 330 335
 Ala Ala Glu Leu Ala Tyr Phe Gly Ala Gln Val Leu His Pro Gln Ser
 340 345 350
 Met Arg Pro Ala Arg Glu Ser Asp Ile Pro Val Arg Val Lys Asn Ser
 355 360 365
 Tyr Asn Pro Lys Ala Pro Gly Thr Leu Ile Thr Lys Ala Arg Asp Met
 370 375 380
 Ser Lys Ala Val Leu Thr Ser Ile Val Leu Lys Arg Asn Val Thr Met
 385 390 395 400
 Leu Asp Ile Ala Ser Thr Arg Met Leu Gly Gln Tyr Gly Phe Leu Ala
 405 410 415
 Lys Val Phe Ser Ile Phe Glu Glu Leu Gly Ile Ser Val Asp Val Val
 420 425 430
 Ala Thr Ser Glu Val Ser Val Ser Leu Thr Leu Asp Pro Ser Lys Leu
 435 440 445
 Trp Ser Arg Glu Leu Ile Gln Gln Ala Ser Glu Leu Asp His Val Val
 450 455 460
 Glu Glu Leu Glu Lys Ile Ala Val Val Asn Leu Leu Gln Asn Arg Ser
 465 470 475 480
 Ile Ile Ser Leu Ile Gly Asn Val Gln Arg Ser Ser Leu Ile Leu Glu
 485 490 495
 Arg Leu Ser Arg Val Leu Arg Thr Leu Gly Val Thr Val Gln Met Ile
 500 505 510
 Ser Gln Gly Ala Ser Lys Val Asn Ile Ser Leu Val Val Asn Asp Ser
 515 520 525

Glu Ala Glu Gln Cys Val Arg Ala Leu His Ser Ala Phe Phe Glu Ser
530 535 540

Glu Leu Ser Glu Leu Glu Met Asp Tyr Lys Asn Gly Asn Gly Ser Val
545 550 555 560

Asp Glu Leu Ser

<210> 18

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 18

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17

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 19

gactggtaacc tcagccccacg agtaggt

27

<210> 20

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20

gactccatgg agggattggg gga

23

<210> 21

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21

gttttccccca tggcagaga

19

<210> 22

<211> 32

<212> DNA

<213> Artificial Sequence

PCT/US00/34396

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<220>
<223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 22
ttagtgtttc tgtgttactt gatccatcaa ag 32

<210> 23
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 23
ctttgatgga tcaagtaaca cagaaaacact aac 33

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic oligonucleotide

<400> 24
gactccatgg caatcccagt gcg 23
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